

**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

1. (canceled)
2. (currently amended) A method for determining whether a beagle dog is an extensive metabolizer or a poor metabolizer in the rate of drug metabolism, said method comprising:

preparing a nucleic acid sample from a beagle dog,  
analyzing a base corresponding to a base at position 1117 of a beagle CYP1A2 gene position 1179 of the nucleotide sequence of SEQ ID NO: 22,  
determining the aCYP1A2 genotype at the base corresponding to athe base at position 1117 of the beagle CYP1A2 gene position 1179 of the nucleotide sequence of SEQ ID NO: 22, and  
determining whether judging the beagle dog with a C/C genotype or a C/T genotype to be is an extensive metabolizer and the beagle dog with a T/T genotype to be or a poor metabolizer according to the CYP1A2 genotype.
3. (currently amended) A method for selecting a beagle dog used in a medicament test, comprising

determining whether a beagle dog is an extensive metabolizer or a poor metabolizer in the rate of drug metabolism by the method according to claim 2, and  
selecting a beagle dog that is with a C/C genotype or a C/T genotype as the an extensive metabolizer or a beagle that is dog with a T/T genotype as the a poor metabolizer.

4. (previously presented) A method for assaying a pharmacological effect and/or toxicity of a test drug, comprising

administering a test drug to an extensive metabolizer group or a poor metabolizer group selected by the method according to claim 3, and  
assaying a pharmacological effect and/or toxicity of the test drug.

5 - 9. (canceled)

10. (currently amended) The method according to ~~claim 9-claim 3~~, wherein a beagle dog with the C/C genotype is selected.

11 - 14. (canceled)